

10/581570

SEQUENCE LISTING
AP20 Rec'd PCT/PTO 02 JUN 2006

<110> Liao et al.

<120> PRODUCTION OF 3-HYDROXYPROPIONIC ACID USING BETA
-ALANINE/PYRUVATE AMINOTRANSFERASE

<130> 66576-05

<150> PCT/US2004/040827

<151> 2004-12-06

<150> US 60/527,357

<151> 2003-12-04

<160> 28

<170> PatentIn version 3.2

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ctg gac gcc cac tgg atg ccc tac acc gcc aac cgc aac ttc cag cgc			96
Leu Asp Ala His Trp Met Pro Tyr Thr Ala Asn Arg Asn Phe Gln Arg			
20 25 30			
gac cca cgc ctg atc gtg gcg gcc gaa ggc aac tac ctg gtc gat gac			144
Asp Pro Arg Leu Ile Val Ala Ala Glu Gly Asn Tyr Leu Val Asp Asp			
35 40 45			
cac ggg cgc aag atc ttc gac gcc ctg tcc ggc ctg tgg acc tgc ggc			192
His Gly Arg Lys Ile Phe Asp Ala Leu Ser Gly Leu Trp Thr Cys Gly			
50 55 60			
gca ggg cac act cgc aag gaa atc gct gac gcg gtg acc cgt caa ctg			240
Ala Gly His Thr Arg Lys Glu Ile Ala Asp Ala Val Thr Arg Gln Leu			
65 70 75 80			
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Ser Thr Leu Asp Tyr Ser Pro Ala Phe Gln Phe Gly His Pro Leu Ser			
85 90 95			
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Phe Gln Leu Ala Glu Lys Ile Ala Glu Leu Val Pro Gly Asn Leu Asn			
100 105 110			
cac gtc ttc tat acc aac tcc ggt tcc gag tgc gcc gat acc gca ctg			384
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130 135 140			
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Lys Ile Ile Gly Arg Ala Arg Gly Tyr His Gly Val Asn Ile Ala Gly			
145 150 155 160			
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Thr Ser Leu Gly Gly Val Asn Gly Asn Arg Lys Met Phe Gly Gln Leu			
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Leu Asp Val Asp His Leu Pro His Thr Val Leu Pro Val Asn Ala Phe			
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tcg aaa ggc ttg ccg gaa gag ggc ggt atc gcg ctg gct gac gaa atg			624
Ser Lys Gly Leu Pro Glu Glu Gly Gly Ile Ala Leu Ala Asp Glu Met			
195 200 205			
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Leu Lys Leu Ile Glu Leu His Asp Ala Ser Asn Ile Ala Ala Val Ile			
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Tyr Leu Lys Arg Leu Arg Glu Ile Cys Thr Gln His Asn Ile Leu Leu			
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ggc tcg gaa gcc ttc ggc gtt acc ccg gac ctg atg tgc atc gcc aag			864
Gly Ser Glu Ala Phe Gly Val Thr Pro Asp Leu Met Cys Ile Ala Lys			
275	280	285	
cag gtg acc aac ggc gcc atc ccg atg ggc gca gtg att gcc agc agc			912
Gln Val Thr Asn Gly Ala Ile Pro Met Gly Ala Val Ile Ala Ser Ser			
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Glu Ile Tyr Gln Thr Phe Met Asn Gln Pro Thr Pro Glu Tyr Ala Val			
305	310	315	320
gaa ttc cca cac ggc tac acc tat tcg gcg cac ccg gta gcc tgt gcc			1008
Glu Phe Pro His Gly Tyr Thr Tyr Ser Ala His Pro Val Ala Cys Ala			
325	330	335	
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Ala Gly Leu Ala Ala Leu Asp Leu Leu Gln Lys Glu Asn Leu Val Gln			
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tcc gcg gct gaa ctg gcg ccg cat ttc gag aag ctg ctg cac ggc gtg			1104
Ser Ala Ala Glu Leu Ala Pro His Phe Glu Lys Leu Leu His Gly Val			
355	360	365	
aag ggc acc aag aat atc gtc gat atc cgc aac tac ggc ctg gcc ggc			1152
Lys Gly Thr Lys Asn Ile Val Asp Ile Arg Asn Tyr Gly Leu Ala Gly			
370	375	380	
gcc atc cag atc gcc gcc cgt gac ggt gat gcc atc gtt cgc cct tac			1200
Ala Ile Gln Ile Ala Ala Arg Asp Gly Asp Ala Ile Val Arg Pro Tyr			
385	390	395	400
gaa gcg gcc atg aag ctg tgg aaa gcg ggc ttc tat gta cgc ttt ggt			1248
Glu Ala Ala Met Lys Leu Trp Lys Ala Gly Phe Tyr Val Arg Phe Gly			
405	410	415	
ggc gac acc ctg cag ttc ggc cca acc ttc aat acc aag ccg cag gaa			1296
Gly Asp Thr Leu Gln Phe Gly Pro Thr Phe Asn Thr Lys Pro Gln Glu			
420	425	430	
ctg gac cgc ttg ttc gat gct gtt ggc gaa acc ctg aac ctg atc gac			1344
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435

440

445

tga

1347

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35 40 45

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Phe Gln Leu Ala Glu Lys Ile Ala Glu Leu Val Pro Gly Asn Leu Asn
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Leu Asp Val Asp His Leu Pro His Thr Val Leu Pro Val Asn Ala Phe

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185

190

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210 215 220

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Glu Phe Pro His Gly Tyr Thr Tyr Ser Ala His Pro Val Ala Cys Ala
325 330 335

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Ser Ala Ala Glu Leu Ala Pro His Phe Glu Lys Leu Leu His Gly Val
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Leu Arg Ala His Trp Met Pro Phe Ser Ala Asn Arg Asn Phe Gln Lys
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Asp Pro Arg Ile Ile Val Ala Ala Glu Gly Ser Trp Leu Thr Asp Asp
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Lys Gly Arg Lys Val Tyr Asp Ser Leu Ser Gly Leu Trp Thr Cys Gly
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Gly Thr Leu Asp Tyr Ser Pro Gly Phe Gln Tyr Gly His Pro Leu Ser
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Phe Gln Leu Ala Glu Lys Ile Ala Gly Leu Leu Pro Gly Glu Leu Asn
100 105 110

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100 105 110																

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Met Asp Val Asp His Leu Pro His Thr Leu Gln Pro Gly Met Ala Phe
180 185 190

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195 200 205

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210 215 220

Val Glu Pro Met Ser Gly Ser Ala Gly Val Leu Val Pro Pro Val Gly
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Tyr Leu Gln Arg Leu Arg Glu Ile Cys Asp Gln His Asn Ile Leu Leu
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260 265 270

Gly Ala Glu Tyr Phe Gly Val Thr Pro Asp Leu Met Asn Val Ala Lys
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Gln Val Thr Asn Gly Ala Val Pro Met Gly Ala Val Ile Ala Ser Ser
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Glu Ile Tyr Asp Thr Phe Met Asn Gln Ala Leu Pro Glu His Ala Val
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325 330 335

Ala Gly Leu Ala Ala Leu Asp Ile Leu Ala Arg Asp Asn Leu Val Gln

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345

350

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Glu Ala Gly Met Lys Leu Trp Gln Gln Gly Phe Tyr Val Arg Phe Gly
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Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln
20 25 30

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35 40 45

ctg acc gag gat gaa gag gaa ggc gtc cgt att tct acc aaa acg atc 192
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50 55 60

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65 70 75 80

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gta aaa atc aga gtc cgt cct tat tat att tac caa tgt gat ctg tca Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser 290 295 300	912

gaa gga ata ggg cat ttc cgt gct cct gtt tcc aaa ggt ttg gag atc Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile 305 310 315 320	960
att gaa ggg ctg aga ggt cat acc tca ggc tat gcg gtt cct acc ttt Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe 325 330 335	1008
gtc gtt cac gca cca ggc gga gga ggt aaa atc gcc ctg cag ccg aac Val Val His Ala Pro Gly Gly Lys Ile Ala Leu Gln Pro Asn 340 345 350	1056
tat gtc ctg tca caa agt cct gac aaa gtg atc tta aga aat ttt gaa Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu 355 360 365	1104
ggt gtg att acg tca tat ccg gaa cca gag aat tat atc ccc aat cag Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln 370 375 380	1152
gca gac gcc tat ttt gag tcc gtt ttc cct gaa acc gct gac aaa aag Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys 385 390 395 400	1200
gag ccg atc ggg ctg agt gcc att ttt gct gac aaa gaa gtt tcg ttt Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe 405 410 415	1248
aca cct gaa aat gta gac aga atc aaa cgg cgt gag gca tac atc gca Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala 420 425 430	1296
aat ccg gag cat gaa aca tta aaa gat cgg cgt gag aaa aga gat cag Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln 435 440 445	1344
ctc aaa gaa aag aaa ttt ttg gcg cag cag aaa aaa cag aaa gag act Leu Lys Glu Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr 450 455 460	1392
gaa tgc gga ggg gat tct tca tga Glu Cys Gly Gly Asp Ser Ser 465 470	1416
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<211> 471	
<212> PRT	
<213> Bacillus subtilis	
<400> 22	
Met Lys Asn Lys Trp Tyr Lys Pro Lys Arg His Trp Lys Glu Ile Glu 1 5 10 15	
Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln	

20

25

30

Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn
 35 40 45

Leu Thr Glu Asp Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile
 50 55 60

Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn
 65 70 75 80

Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met
 85 90 95

His Lys Thr Lys Tyr Asp Met Glu Asp Pro Leu His Glu Asp Glu Asp
 100 105 110

Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe
 115 120 125

Leu Val Thr Asn Gln Cys Ser Val Tyr Cys Arg His Cys Thr Arg Arg
 130 135 140

Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp
 145 150 155 160

Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu
 165 170 175

Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr
 180 185 190

Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile
 195 200 205

Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu
 210 215 220

Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe
 225 230 235 240

Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys
 245 250 255

Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala
260 265 270

Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu
275 280 285

Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser
290 295 300

Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile
305 310 315 320

Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe
325 330 335

Val Val His Ala Pro Gly Gly Gly Lys Ile Ala Leu Gln Pro Asn
340 345 350

Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu
355 360 365

Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln
370 375 380

Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys
385 390 395 400

Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe
405 410 415

Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala
420 425 430

Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln
435 440 445

Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr
450 455 460

Glu Cys Gly Gly Asp Ser Ser
465 470

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 <211> 1416
 <212> DNA
 <213> Bacillus subtilis

<220>
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atg aaa aac aaa tgg tat aaa ccg aaa cgg cat tgg aag gag atc gag		48	
Met Lys Asn Lys Trp Tyr Lys Pro Lys Arg His Trp Lys Glu Ile Glu			
1	5	10	15
tta tgg aag gac gtt ccg gaa gag aaa tgg aac gat tgg ctt tgg cag			96
Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln			
20	25	30	
ctg aca cac act gta aga acg tta gat gat tta aag aaa gtc att aat			144
Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Val Ile Asn			
35	40	45	
ctg acc gag gat gaa gag gaa ggc gtc aga att tct acc aaa acg atc			192
Leu Thr Glu Asp Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile			
50	55	60	
ccc tta aat att aca cct tac tat gct tct tta atg gac ccc gac aat			240
Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn			
65	70	75	80
ccg aga tgc ccg gta cgc atg cag tct gtg ccg ctt tct gaa gaa atg			288
Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met			
85	90	95	
cac aaa aca aaa tac gat atg gaa gac ccg ctt cat gag gat gaa gat			336
His Lys Thr Lys Tyr Asp Met Glu Asp Pro Leu His Glu Asp Glu Asp			
100	105	110	
tca ccg gta ccc ggt ctg aca cac cgc tat ccc gac cgt gtg ctg ttt			384
Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe			
115	120	125	
ctt gtc acg aat caa tgt tcc gtg tac tgc cgc tac tgc aca aga agg			432
Leu Val Thr Asn Gln Cys Ser Val Tyr Cys Arg Tyr Cys Thr Arg Arg			
130	135	140	
cgc ttt tcc gga caa atc gga atg ggc gtc ccc aaa aaa cag ctt gat			480
Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp			
145	150	155	160
gct gca att gct tat atc cgg gaa aca ccc gaa atc cgc gat tgt tta			528
Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu			
165	170	175	
att tca ggc ggt gat ggg ctg ctc atc aac gac caa att tta gaa tat			576

Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr			
180	185	190	
att tta aaa gag ctg cgc agc att ccg cat ctg gaa gtc atc aga atc			624
Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile			
195	200	205	
gga aca aca gct ccc gtc gtc ttt ccg cag cgc att acc gat cat ctg			672
Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu			
210	215	220	
tgc gag ata ttg aaa aaa tat cat ccg gtc tgg ctg aac acc cat ttt			720
Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe			
225	230	235	240
aac aca agc atc gaa atg aca gaa tcc gtt gag gca tgt gaa aag			768
Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys			
245	250	255	
ctg gtg aac gcg gga gtg ccg gtc gga aat cag gct gtc gta tta gca			816
Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala			
260	265	270	
ggt att aat gat tcg gtt cca att atg aaa aag ctc atg cat gac ttg			864
Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu			
275	280	285	
gta aaa atc aga gtc cgt cct tat tat att tac caa tgt gat ctg tca			912
Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser			
290	295	300	
gaa gga ata ggg cat ttc aga gct cct gtt tcc aaa ggt ttg gag atc			960
Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile			
305	310	315	320
att gaa ggg ctg aga ggt cat acc tca ggc tat gcg gtt cct acc ttt			1008
Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe			
325	330	335	
gtc gtt cac gca cca ggc gga ggt aaa atc gcc ctg cag ccg aac			1056
Val Val His Ala Pro Gly Gly Lys Ile Ala Leu Gln Pro Asn			
340	345	350	
tat gtc ctg tca caa agt cct gac aaa gtg atc tta aga aat ttt gaa			1104
Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu			
355	360	365	
ggt gtg att acg tca tat ccg gaa cca gag aat tat atc ccc aat cag			1152
Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln			
370	375	380	
gca gac gcc tat ttt gag tcc gtt ttc cct gaa acc gct gac aaa aag			1200
Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys			
385	390	395	400
gag ccg atc ggg ctg agt gcc att ttt gct gac aaa gaa gtt tcg ttt			1248
Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe			

405	410	415	
aca cct gaa aat gta gac aga atc aaa agg aga gag gca tac atc gca Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala			1296
420	425	430	
aat ccg gag cat gaa aca tta aaa gat cgg cgt gag aaa aga gat cag Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln			1344
435	440	445	
ctc aaa gaa aag aaa ttt ttg gcg cag cag aaa aaa cag aaa gag act Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr			1392
450	455	460	
gaa tgc gga ggg gat tct tca tga Glu Cys Gly Gly Asp Ser Ser			1416
465	470		
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<212> PRT			
<213> Bacillus subtilis			
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Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln 20 25 30			
Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn 35 40 45			
Leu Thr Glu Asp Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile 50 55 60			
Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn 65 70 75 80			
Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met 85 90 95			
His Lys Thr Lys Tyr Asp Met Glu Asp Pro Leu His Glu Asp Glu Asp 100 105 110			
Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe 115 120 125			

Leu Val Thr Asn Gln Cys Ser Val Tyr Cys Arg Tyr Cys Thr Arg Arg
130 135 140

Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp
145 150 155 160

Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu
165 170 175

Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr
180 185 190

Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile
195 200 205

Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu
210 215 220

Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe
225 230 235 240

Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys
245 250 255

Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala
260 265 270

Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu
275 280 285

Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser
290 295 300

Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile
305 310 315 320

Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe
325 330 335

Val Val His Ala Pro Gly Gly Lys Ile Ala Leu Gln Pro Asn
340 345 350

Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu
355 360 365

Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln
370 375 380

Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys
385 390 395 400

Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe
405 410 415

Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala
420 425 430

Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln
435 440 445

Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr
450 455 460

Glu Cys Gly Gly Asp Ser Ser
465 470

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<211> 1251
<212> DNA
<213> Porphyromonas gingivalis

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<221> CDS
<222> (1)..(1248)

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Met Ala Glu Ser Arg Arg Lys Tyr Tyr Phe Pro Asp Val Thr Asp Glu
1 5 10 15

caa tgg tac gac tgg cat tgg cag gtc ctc aat cga att gag acg ctc 96
Gln Trp Tyr Asp Trp His Trp Gln Val Leu Asn Arg Ile Glu Thr Leu
20 25 30

gac cag ctg aaa aag tac gtt aca ctc acc gct gaa gaa gag gga 144
Asp Gln Leu Lys Tyr Val Thr Leu Thr Ala Glu Glu Glu Gly
35 40 45

gta aaa gaa tcg ccc aaa gta ctc cga atg gct atc aca cct tat tat 192
Val Lys Glu Ser Pro Lys Val Leu Arg Met Ala Ile Thr Pro Tyr Tyr

50	55	60	
ttg agt ttg ata gac ccc gag aat cct aat tgt ccg att cgt aaa caa Leu Ser Leu Ile Asp Pro Glu Asn Pro Asn Cys Pro Ile Arg Lys Gln	65	70	240
65	70	75	80
gcc att cct actcaa cag gaa ctg gta cgt gct cct gaa gat cag gta Ala Ile Pro Thr Gln Gln Glu Leu Val Arg Ala Pro Glu Asp Gln Val	85	90	288
85	90	95	
gac cca ctt agt gaa gat gaa gat tcg ccc gta ccc gga ctg act cat Asp Pro Leu Ser Glu Asp Glu Asp Ser Pro Val Pro Gly Leu Thr His	100	105	336
100	105	110	
cgt tat ccg gat cgt gta ttg ttc ctt atc acg gac aaa tgt tcg atg Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met	115	120	384
115	120	125	
tac tgt cgt cat tgt act cgc cgt cgc ttc gca gga cag aaa gat gct Tyr Cys Arg His Cys Thr Arg Arg Phe Ala Gly Gln Lys Asp Ala	130	135	432
130	135	140	
tct tct cct gag cgc atc gat cga tgc att gac tat ata gcc aat Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn	145	150	480
145	150	155	160
aca ccg aca gtc cgc gat gtt ttg cta tcg gga ggc gat gcc ctc ctt Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu	165	170	528
165	170	175	
gtc agc gac gaa cgc ttg gaa tac ata ttg aag cgt ctg cgc gaa ata Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile	180	185	576
180	185	190	
cct cat gtg gag att gtt cgt ata gga agc cgt acg ccg gta gtc ctc Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu	195	200	624
195	200	205	
cct cag cgt ata acg cct caa ttg gtg gat atg ctc aaa aaa tat cat Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His	210	215	672
210	215	220	
ccg gtg tgg ctg aac act cac ttc aac cac ccg aat gaa gtt acc gaa Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu	225	230	720
225	230	235	240
gaa gca gta gag gct tgt gaa aga atg gcc aat gcc ggt att ccg ttg Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu	245	250	768
245	250	255	
ggt aac caa acg gtt tta ttg cgt gga atc aat gat tgt aca cat gtg Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val	260	265	816
260	265	270	
atg aag aga ttg gta cat ttg ctg gta aag atg cgt gtg cgt cct tac Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr	275	280	864
275	280	285	

tat ata tat gta tgc gat ctt tcg ctt gga ata ggt cat ttc cgc acg Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr 290 295 300	912
ccg gta tct aaa gga atc gaa att atc gaa aat ttg cgc gga cac acc Pro Val Ser Lys Gly Ile Glu Ile Glu Asn Leu Arg Gly His Thr 305 310 315 320	960
tcg ggc tat gca gtt cct acc ttt gtg gta ggt gct ccg ggg ggt ggt Ser Gly Tyr Ala Val Pro Thr Phe Val Val Gly Ala Pro Gly Gly 325 330 335	1008
ggt aag ata cct gta acg ccg aac tat gtt gta tct cag tcc cca cga Gly Lys Ile Pro Val Thr Pro Asn Tyr Val Val Ser Gln Ser Pro Arg 340 345 350	1056
cat gtg gtt ctt cgc aat tat gaa ggt gtt atc aca acc tat acg gag His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu 355 360 365	1104
ccg gag aat tat cat gag gag tgc gat tgt gag gac tgt cga gcc ggt Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly 370 375 380	1152
aag cat aaa gag ggt gta gct gca ctt tcc gga ggt cag cag ttg gct Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala 385 390 395 400	1200
atc gag cct tcc gac tta gct cgc aaa aaa cgc aag ttt gat aag aac Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn 405 410 415	1248
tga	1251

<210> 26
<211> 416
<212> PRT
<213> Porphyromonas gingivalis

<400> 26

Met Ala Glu Ser Arg Arg Lys Tyr Tyr Phe Pro Asp Val Thr Asp Glu
1 5 10 15

Gln Trp Tyr Asp Trp His Trp Gln Val Leu Asn Arg Ile Glu Thr Leu
20 25 30

Asp Gln Leu Lys Lys Tyr Val Thr Leu Thr Ala Glu Glu Glu Gly
35 40 45

Val Lys Glu Ser Pro Lys Val Leu Arg Met Ala Ile Thr Pro Tyr Tyr
50 55 60

Leu Ser Leu Ile Asp Pro Glu Asn Pro Asn Cys Pro Ile Arg Lys Gln
65 70 75 80

Ala Ile Pro Thr Gln Gln Glu Leu Val Arg Ala Pro Glu Asp Gln Val
85 90 95

Asp Pro Leu Ser Glu Asp Glu Asp Ser Pro Val Pro Gly Leu Thr His
100 105 110

Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met
115 120 125

Tyr Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Lys Asp Ala
130 135 140

Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn
145 150 155 160

Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu
165 170 175

Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile
180 185 190

Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu
195 200 205

Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His
210 215 220

Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu
225 230 235 240

Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu
245 250 255

Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val
260 265 270

Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr
275 280 285

Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr
290 295 300

Pro Val Ser Lys Gly Ile Glu Ile Glu Asn Leu Arg Gly His Thr
305 310 315 320

Ser Gly Tyr Ala Val Pro Thr Phe Val Val Gly Ala Pro Gly Gly Gly
325 330 335

Gly Lys Ile Pro Val Thr Pro Asn Tyr Val Val Ser Gln Ser Pro Arg
340 345 350

His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu
355 360 365

Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly
370 375 380

Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala
385 390 395 400

Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn
405 410 415

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<211> 897
<212> DNA
<213> Pseudomonas aeruginosa

<220>
<221> CDS
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<400> 27
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Met Thr Asp Ile Ala Phe Leu Gly Leu Gly Asn Met Gly Gly Pro Met
1 5 10 15

gcc gcc aac ctg ctc aag gcc ggc cac cggt gtg aat gtc ttc gac ttg 96
Ala Ala Asn Leu Leu Lys Ala Gly His Arg Val Asn Val Phe Asp Leu
20 25 30

cag ccc aag gcc gtg ctg ggc ctg gtc gag cag ggc gcg cag ggc gcc 144
Gln Pro Lys Ala Val Leu Gly Leu Val Glu Gln Gly Ala Gln Gly Ala
35 40 45

gat agc gcc ttg cag tgc tgc gaa ggc gcc gaa gtg gtg atc agc atg 192

Asp Ser Ala Leu Gln Cys Cys Glu Gly Ala Glu Val Val Ile Ser Met			
50	55	60	
ctg ccg gcc ggg cag cac gtg gaa agc ctg tat ctc ggc gac gac ggc			240
Leu Pro Ala Gly Gln His Val Glu Ser Leu Tyr Leu Gly Asp Asp Gly			
65	70	75	80
ctg ctc gcg cgg gtc gcc ggc aag ccc ctg ctg atc gac tgc tcg acc			288
Leu Leu Ala Arg Val Ala Gly Lys Pro Leu Leu Ile Asp Cys Ser Thr			
85	90	95	
atc gcc ccg gag acc gcg cgc aag gtc gcc gag gcc gcc gcg gcg aag			336
Ile Ala Pro Glu Thr Ala Arg Lys Val Ala Glu Ala Ala Ala Lys			
100	105	110	
ggc ctg acc ctg ctc gac gcg ccg gtt tcc ggc ggc gtc ggc ggc gcc			384
Gly Leu Thr Leu Leu Asp Ala Pro Val Ser Gly Gly Val Gly Gly Ala			
115	120	125	
cgc gcc ggc acc ctg agc ttc atc gtc ggc ggc ccc gcc gaa ggc ttc			432
Arg Ala Gly Thr Leu Ser Phe Ile Val Gly Gly Pro Ala Glu Gly Phe			
130	135	140	
gcf cgg gcc cgg ccg gtc ctc gag aac atg ggc cgg aac atc ttc cac			480
Ala Arg Ala Arg Pro Val Leu Glu Asn Met Gly Arg Asn Ile Phe His			
145	150	155	160
gcc ggc gat cac ggc gcc ggc cag gtg gcg aag atc tgc aac aac atg			528
Ala Gly Asp His Gly Ala Gly Gln Val Ala Lys Ile Cys Asn Asn Met			
165	170	175	
ctc ctc ggc atc ctc atg gcc ggc acc gcc gag gcc ctg gcg ctg ggg			576
Leu Leu Gly Ile Leu Met Ala Gly Thr Ala Glu Ala Leu Ala Leu Gly			
180	185	190	
gtg aag aac ggc ctc gac ccg gcg gtg ctg tcc gag gtg atg aag cag			624
Val Lys Asn Gly Leu Asp Pro Ala Val Leu Ser Glu Val Met Lys Gln			
195	200	205	
agt tcc ggc ggc aac tgg gcg ctg aac ctc tac aac ccc tgg ccc ggg			672
Ser Ser Gly Asn Trp Ala Leu Asn Leu Tyr Asn Pro Trp Pro Gly			
210	215	220	
gtg atg ccg cag gcg ccg gcg agc aac ggc tat gcc ggc ggt ttc cag			720
Val Met Pro Gln Ala Pro Ala Ser Asn Gly Tyr Ala Gly Gly Phe Gln			
225	230	235	240
gtg cgc ctg atg aac aag gac ctc ggc ctg gcg ctg gcc aac gcc cag			768
Val Arg Leu Met Asn Lys Asp Leu Gly Leu Ala Leu Ala Asn Ala Gln			
245	250	255	
gcf gtg cag gcc tcg acg ccg ctc ggc gcg ctg gcg cgc aac ctg ttc			816
Ala Val Gln Ala Ser Thr Pro Leu Gly Ala Leu Ala Arg Asn Leu Phe			
260	265	270	
agc ctg cac gcc cag gcc gat gcc gag cac gag ggg ctg gac ttc tcc			864
Ser Leu His Ala Gln Ala Asp Ala Glu His Glu Gly Leu Asp Phe Ser			

275

280

285

agc atc cag aag ctc tac cgc ggc aag gac taa
 Ser Ile Gln Lys Leu Tyr Arg Gly Lys Asp
 290 295

897

<210> 28
 <211> 298
 <212> PRT
 <213> Pseudomonas aeruginosa

<400> 28

Met Thr Asp Ile Ala Phe Leu Gly Leu Gly Asn Met Gly Gly Pro Met
 1 5 10 15

Ala Ala Asn Leu Leu Lys Ala Gly His Arg Val Asn Val Phe Asp Leu
 20 25 30

Gln Pro Lys Ala Val Leu Gly Leu Val Glu Gln Gly Ala Gln Gly Ala
 35 40 45

Asp Ser Ala Leu Gln Cys Cys Glu Gly Ala Glu Val Val Ile Ser Met
 50 55 60

Leu Pro Ala Gly Gln His Val Glu Ser Leu Tyr Leu Gly Asp Asp Gly
 65 70 75 80

Leu Leu Ala Arg Val Ala Gly Lys Pro Leu Leu Ile Asp Cys Ser Thr
 85 90 95

Ile Ala Pro Glu Thr Ala Arg Lys Val Ala Glu Ala Ala Ala Lys
 100 105 110

Gly Leu Thr Leu Leu Asp Ala Pro Val Ser Gly Gly Val Gly Gly Ala
 115 120 125

Arg Ala Gly Thr Leu Ser Phe Ile Val Gly Gly Pro Ala Glu Gly Phe
 130 135 140

Ala Arg Ala Arg Pro Val Leu Glu Asn Met Gly Arg Asn Ile Phe His
 145 150 155 160

Ala Gly Asp His Gly Ala Gly Gln Val Ala Lys Ile Cys Asn Asn Met
 165 170 175

Leu Leu Gly Ile Leu Met Ala Gly Thr Ala Glu Ala Leu Ala Leu Gly
180 185 190

Val Lys Asn Gly Leu Asp Pro Ala Val Leu Ser Glu Val Met Lys Gln
195 200 205

Ser Ser Gly Gly Asn Trp Ala Leu Asn Leu Tyr Asn Pro Trp Pro Gly
210 215 220

Val Met Pro Gln Ala Pro Ala Ser Asn Gly Tyr Ala Gly Gly Phe Gln
225 230 235 240

Val Arg Leu Met Asn Lys Asp Leu Gly Leu Ala Leu Ala Asn Ala Gln
245 250 255

Ala Val Gln Ala Ser Thr Pro Leu Gly Ala Leu Ala Arg Asn Leu Phe
260 265 270

Ser Leu His Ala Gln Ala Asp Ala Glu His Glu Gly Leu Asp Phe Ser
275 280 285

Ser Ile Gln Lys Leu Tyr Arg Gly Lys Asp
290 295